

## SEQUENCE LISTING

&lt;110&gt; BASF Aktiengesellschaft

&lt;120&gt; Process for the biotransformation of carotenoids

&lt;130&gt; M43191 beta-Karotin Biotransformation

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 12

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1170

&lt;212&gt; DNA

&lt;213&gt; Thermus thermophilus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1170)

&lt;400&gt; 1

atg	aag	cgc	ctt	tcc	ctg	agg	gag	gcc	tgg	ccc	tac	ctg	aaa	gac	ctc	48
Met	Lys	Arg	Leu	Ser	Leu	Arg	Glu	Ala	Trp	Pro	Tyr	Leu	Lys	Asp	Leu	
1				5					10					15		

cag	caa	gat	ccc	ctc	gcc	gtc	ctg	ctg	gcg	tgg	ggc	cgg	gcc	cac	ccc	96
Gln	Gln	Asp	Pro	Leu	Ala	Val	Leu	Leu	Ala	Trp	Gly	Arg	Ala	His	Pro	
			20					25					30			

cgg	ctc	ttc	ctt	ccc	ctg	ccc	cgc	ttc	ccc	ctg	gcc	ctg	atc	ttt	gac	144
Arg	Leu	Phe	Leu	Pro	Leu	Pro	Arg	Phe	Pro	Leu	Ala	Leu	Ile	Phe	Asp	
		35					40					45				

ccc	gag	ggg	gtg	gag	ggg	gcg	ctc	ctc	gcc	gag	ggg	acc	acc	aag	gcc	192
Pro	Glu	Gly	Val	Glu	Gly	Ala	Leu	Leu	Ala	Glu	Gly	Thr	Thr	Lys	Ala	
	50					55					60					

acc	ttc	cag	tac	cgg	gcc	ctc	tcc	cgc	ctc	acg	ggg	agg	ggc	ctc	ctc	240
Thr	Phe	Gln	Tyr	Arg	Ala	Leu	Ser	Arg	Leu	Thr	Gly	Arg	Gly	Leu	Leu	
	65				70					75					80	

acc	gac	tgg	ggg	gaa	agc	tgg	aag	gag	gcg	cgc	aag	gcc	ctc	aaa	gac	288
Thr	Asp	Trp	Gly	Glu	Ser	Trp	Lys	Glu	Ala	Arg	Lys	Ala	Leu	Lys	Asp	
			85						90					95		

ccc	ttc	ctg	ccg	aag	aac	gtc	cgc	ggc	tac	cgg	gag	gcc	atg	gag	gag	336
Pro	Phe	Leu	Pro	Lys	Asn	Val	Arg	Gly	Tyr	Arg	Glu	Ala	Met	Glu	Glu	
		100						105					110			

gag	gcc	cgg	gcc	ttc	ttc	ggg	gag	tgg	cgg	ggg	gag	gag	cgg	gac	ctg	384
Glu	Ala	Arg	Ala	Phe	Phe	Gly	Glu	Trp	Arg	Gly	Glu	Glu	Arg	Asp	Leu	
		115				120						125				

gac	cac	gag	atg	ctc	gcc	ctc	tcc	ctg	cgc	ctc	ctc	ggg	cgg	gcc	ctc	432
Asp	His	Glu	Met	Leu	Ala	Leu	Ser	Leu	Arg	Leu	Gly	Arg	Ala	Leu		
	130					135					140					

ttc	ggg	aag	ccc	ctc	tcc	cca	agc	ctc	gcg	gag	cac	gcc	ctt	aag	gcc	480
Phe	Gly	Lys	Pro	Leu	Ser	Pro	Ser	Leu	Ala	Glu	His	Ala	Leu	Lys	Ala	

145	150	155	160	
ctg gac cgg atc atg gcc cag acc agg agc ccc ctg gcc ctc ctg gac				528
Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp				
	165	170	175	
ctg gcc gcc gaa gcc cgc ttc cgg aag gac cgg ggg gcc ctc tac cgc				576
Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg				
	180	185	190	
gag gcg gaa gcc ctc atc gtc cac ccg ccc ctc tcc cac ctt ccc cga				624
Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg				
	195	200	205	
gag cgc gcc ctg agc gag gcc gtg acc ctc ctg gtg gcg ggc cac gag				672
Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu				
	210	215	220	
acg gtg gcg agc gcc ctc acc tgg tcc ttt ctc ctc ctc tcc cac cgc				720
Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg				
	225	230	235	240
ccg gac tgg cag aag cgg gtg gcc gag agc gag gag gcg gcc ctc gcc				768
Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala				
	245	250	255	
gcc ttc cag gag gcc ctg agg ctc tac ccc ccc gcc tgg atc ctc acc				816
Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr				
	260	265	270	
cgg agg ctg gaa agg ccc ctc ctc ctg gga gag gac cgg ctc ccc ccg				864
Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro				
	275	280	285	
ggc acc acc ctg gtc ctc tcc ccc tac gtg acc cag agg ctc cac ttc				912
Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe				
	290	295	300	
ccc gat ggg gag gcc ttc cgg ccc gag cgc ttc ctg gag gaa agg ggg				960
Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly				
	305	310	315	320
acc cct tcg ggg cgc tac ttc ccc ttt ggc ctg ggg cag agg ctc tgc				1008
Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys				
	325	330	335	
ctg ggg cgg gac ttc gcc ctc ctc gag ggc ccc atc gtc ctc agg gcc				1056
Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala				
	340	345	350	
ttc ttc cgc cgc ttc cgc cta gac ccc ctc ccc ttc ccc cgg gtc ctc				1104
Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu				
	355	360	365	
gcc cag gtc acc ctg agg ccc gaa ggc ggg ctt ccc gcg cgg cct agg				1152
Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg				
	370	375	380	
gag gag gtg cgg gcg tga				1170
Glu Glu Val Arg Ala				
	385	390		

<210> 2  
 <211> 389  
 <212> PRT  
 <213> Thermus thermophilus

<400> 2  
 Met Lys Arg Leu Ser Leu Arg Glu Ala Trp Pro Tyr Leu Lys Asp Leu  
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 Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro  
           20                  25                  30  
 Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp  
       35                  40                  45  
 Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala  
       50                  55                  60  
 Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu  
       65                  70                  75                  80  
 Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp  
           85                  90                  95  
 Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu  
           100                  105                  110  
 Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu  
       115                  120                  125  
 Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu  
       130                  135                  140  
 Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala  
       145                  150                  155                  160  
 Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp  
           165                  170                  175  
 Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg  
           180                  185                  190  
 Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg  
       195                  200                  205  
 Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu  
       210                  215                  220  
 Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg  
       225                  230                  235                  240  
 Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala  
           245                  250                  255  
 Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr  
           260                  265                  270  
 Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro  
       275                  280                  285  
 Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe  
       290                  295                  300

Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly  
 305 310 315 320

Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys  
 325 330 335

Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala  
 340 345 350

Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu  
 355 360 365

Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg  
 370 375 380

Glu Glu Val Arg Ala  
 385

<210> 3  
 <211> 1188  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> (4)..(21)  
 <223> His tag

<220>  
 <223> Description of the artificial sequence: N-terminal  
 his tagged

<220>  
 <221> CDS  
 <222> (1)..(1188)

<400> 3  
 atg cat cac cat cat cat cac aag cgc ctt tcc ctg agg gag gcc tgg 48  
 Met His His His His His His Lys Arg Leu Ser Leu Arg Glu Ala Trp  
 1 5 10 15

ccc tac ctg aaa gac ctc cag caa gat ccc ctc gcc gtc ctg ctg gcg 96  
 Pro Tyr Leu Lys Asp Leu Gln Gln Asp Pro Leu Ala Val Leu Leu Ala  
 20 25 30

tgg ggc cgg gcc cac ccc cgg ctc ttc ctt ccc ctg ccc cgc ttc ccc 144  
 Trp Gly Arg Ala His Pro Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro  
 35 40 45

ctg gcc ctg atc ttt gac ccc gag ggg gtg gag ggg gcg ctc ctc gcc 192  
 Leu Ala Leu Ile Phe Asp Pro Glu Gly Val Glu Gly Ala Leu Leu Ala  
 50 55 60

gag ggg acc acc aag gcc acc ttc cag tac cgg gcc ctc tcc cgc ctc 240  
 Glu Gly Thr Thr Lys Ala Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu  
 65 70 75 80

acg ggg agg ggc ctc ctc acc gac tgg ggg gaa agc tgg aag gag gcg 288  
 Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala  
 85 90 95

cgc aag gcc ctc aaa gac ccc ttc ctg ccg aag aac gtc cgc ggc tac	336
Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr	
100 105 110	
cgg gag gcc atg gag gag gag gcc cgg gcc ttc ttc ggg gag tgg cgg	384
Arg Glu Ala Met Glu Glu Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg	
115 120 125	
ggg gag gag cgg gac ctg gac cac gag atg ctc gcc ctc tcc ctg cgc	432
Gly Glu Glu Arg Asp Leu Asp His Glu Met Leu Ala Leu Ser Leu Arg	
130 135 140	
ctc ctc ggg cgg gcc ctc ttc ggg aag ccc ctc tcc cca agc ctc gcg	480
Leu Leu Gly Arg Ala Leu Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala	
145 150 155 160	
gag cac gcc ctt aag gcc ctg gac cgg atc atg gcc cag acc agg agc	528
Glu His Ala Leu Lys Ala Leu Asp Arg Ile Met Ala Gln Thr Arg Ser	
165 170 175	
ccc ctg gcc ctc ctg gac ctg gcc gcc gaa gcc cgc ttc cgg aag gac	576
Pro Leu Ala Leu Leu Asp Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp	
180 185 190	
cgg ggg gcc ctc tac cgc gag gcg gaa gcc ctc atc gtc cac ccg ccc	624
Arg Gly Ala Leu Tyr Arg Glu Ala Glu Ala Leu Ile Val His Pro Pro	
195 200 205	
ctc tcc cac ctt ccc cga gag cgc gcc ctg agc gag gcc gtg acc ctc	672
Leu Ser His Leu Pro Arg Glu Arg Ala Leu Ser Glu Ala Val Thr Leu	
210 215 220	
ctg gtg gcg ggc cac gag acg gtg gcg agc gcc ctc acc tgg tcc ttt	720
Leu Val Ala Gly His Glu Thr Val Ala Ser Ala Leu Thr Trp Ser Phe	
225 230 235 240	
ctc ctc ctc tcc cac cgc ccg gac tgg cag aag cgg gtg gcc gag agc	768
Leu Leu Leu Ser His Arg Pro Asp Trp Gln Lys Arg Val Ala Glu Ser	
245 250 255	
gag gag gcg gcc ctc gcc gcc ttc cag gag gcc ctg agg ctc tac ccc	816
Glu Glu Ala Ala Leu Ala Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro	
260 265 270	
ccc gcc tgg atc ctc acc cgg agg ctg gaa agg ccc ctc ctc ctg gga	864
Pro Ala Trp Ile Leu Thr Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly	
275 280 285	
gag gac cgg ctc ccc ccg ggc acc acc ctg gtc ctc tcc ccc tac gtg	912
Glu Asp Arg Leu Pro Pro Gly Thr Thr Leu Val Leu Ser Pro Tyr Val	
290 295 300	
acc cag agg ctc cac ttc ccc gat ggg gag gcc ttc cgg ccc gag cgc	960
Thr Gln Arg Leu His Phe Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg	
305 310 315 320	
ttc ctg gag gaa agg ggg acc cct tcg ggg cgc tac ttc ccc ttt ggc	1008
Phe Leu Glu Glu Arg Gly Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly	
325 330 335	
ctg ggg cag agg ctc tgc ctg ggg cgg gac ttc gcc ctc ctc gag ggc	1056
Leu Gly Gln Arg Leu Cys Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly	
340 345 350	

ccc atc gtc ctc agg gcc ttc ttc cgc cgc ttc cgc cta gac ccc ctc 1104  
 Pro Ile Val Leu Arg Ala Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu  
           355                                  360                                  365

ccc ttc ccc cgg gtc ctc gcc cag gtc acc ctg agg ccc gaa ggc ggg 1152  
 Pro Phe Pro Arg Val Leu Ala Gln Val Thr Leu Arg Pro Glu Gly Gly  
           370                                  375                                  380

ctt ccc gcg cgg cct agg gag gag gtg cgg gcg tga 1188  
 Leu Pro Ala Arg Pro Arg Glu Glu Val Arg Ala  
           385                                  390                                  395

<210> 4

<211> 395

<212> PRT

<213> Artificial sequence

<223> Description of the artificial sequence: N-terminal  
           his tagged

<400> 4

Met His His His His His His Lys Arg Leu Ser Leu Arg Glu Ala Trp  
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Pro Tyr Leu Lys Asp Leu Gln Gln Asp Pro Leu Ala Val Leu Leu Ala  
                                   20                                  25                                  30

Trp Gly Arg Ala His Pro Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro  
                                   35                                  40                                  45

Leu Ala Leu Ile Phe Asp Pro Glu Gly Val Glu Gly Ala Leu Leu Ala  
           50                                  55                                  60

Glu Gly Thr Thr Lys Ala Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu  
       65                                  70                                  75                                  80

Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala  
                                   85                                  90                                  95

Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr  
                                   100                                  105                                  110

Arg Glu Ala Met Glu Glu Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg  
           115                                  120                                  125

Gly Glu Glu Arg Asp Leu Asp His Glu Met Leu Ala Leu Ser Leu Arg  
       130                                  135                                  140

Leu Leu Gly Arg Ala Leu Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala  
       145                                  150                                  155                                  160

Glu His Ala Leu Lys Ala Leu Asp Arg Ile Met Ala Gln Thr Arg Ser  
                                   165                                  170                                  175

Pro Leu Ala Leu Leu Asp Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp  
                                   180                                  185                                  190

Arg Gly Ala Leu Tyr Arg Glu Ala Glu Ala Leu Ile Val His Pro Pro  
           195                                  200                                  205

Leu Ser His Leu Pro Arg Glu Arg Ala Leu Ser Glu Ala Val Thr Leu  
       210                                  215                                  220

Leu Val Ala Gly His Glu Thr Val Ala Ser Ala Leu Thr Trp Ser Phe  
 225 230 235 240  
 Leu Leu Leu Ser His Arg Pro Asp Trp Gln Lys Arg Val Ala Glu Ser  
 245 250 255  
 Glu Glu Ala Ala Leu Ala Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro  
 260 265 270  
 Pro Ala Trp Ile Leu Thr Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly  
 275 280 285  
 Glu Asp Arg Leu Pro Pro Gly Thr Thr Leu Val Leu Ser Pro Tyr Val  
 290 295 300  
 Thr Gln Arg Leu His Phe Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg  
 305 310 315 320  
 Phe Leu Glu Glu Arg Gly Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly  
 325 330 335  
 Leu Gly Gln Arg Leu Cys Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly  
 340 345 350  
 Pro Ile Val Leu Arg Ala Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu  
 355 360 365  
 Pro Phe Pro Arg Val Leu Ala Gln Val Thr Leu Arg Pro Glu Gly Gly  
 370 375 380  
 Leu Pro Ala Arg Pro Arg Glu Glu Val Arg Ala  
 385 390 395

<210> 5  
 <211> 1188  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> (1168)..(1185)  
 <223> His tag

<220>  
 <223> Description of the artificial sequence: N-terminal  
 His-tagged

<220>  
 <221> CDS  
 <222> (1)..(1188)

<400> 5  
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 Met Lys Arg Leu Ser Leu Arg Glu Ala Trp Pro Tyr Leu Lys Asp Leu  
 1 5 10 15  
 cag caa gat ccc ctc gcc gtc ctg ctg gcg tgg ggc cgg gcc cac ccc 96  
 Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro  
 20 25 30

cg	g	ctc	ttc	ctt	ccc	ctg	ccc	cgc	ttc	ccc	ctg	gcc	ctg	atc	ttt	gac	144
Arg	Leu	Phe	Leu	Pro	Leu	Pro	Arg	Phe	Pro	Leu	Ala	Leu	Ile	Phe	Asp		
	35						40					45					
ccc	gag	ggg	gtg	gag	ggg	gcg	ctc	ctc	gcc	gag	ggg	acc	acc	aag	gcc	192	
Pro	Glu	Gly	Val	Glu	Gly	Ala	Leu	Leu	Ala	Glu	Gly	Thr	Thr	Lys	Ala		
	50					55				60							
acc	ttc	cag	tac	cgg	gcc	ctc	tcc	cgc	ctc	acg	ggg	agg	ggc	ctc	ctc	240	
Thr	Phe	Gln	Tyr	Arg	Ala	Leu	Ser	Arg	Leu	Thr	Gly	Arg	Gly	Leu	Leu		
	65				70				75					80			
acc	gac	tgg	ggg	gaa	agc	tgg	aag	gag	gcg	cgc	aag	gcc	ctc	aaa	gac	288	
Thr	Asp	Trp	Gly	Glu	Ser	Trp	Lys	Glu	Ala	Arg	Lys	Ala	Leu	Lys	Asp		
				85				90						95			
ccc	ttc	ctg	ccg	aag	aac	gtc	cgc	ggc	tac	cgg	gag	gcc	atg	gag	gag	336	
Pro	Phe	Leu	Pro	Lys	Asn	Val	Arg	Gly	Tyr	Arg	Glu	Ala	Met	Glu	Glu		
			100					105					110				
gag	gcc	cgg	gcc	ttc	ttc	ggg	gag	tgg	cgg	ggg	gag	gag	cgg	gac	ctg	384	
Glu	Ala	Arg	Ala	Phe	Phe	Gly	Glu	Trp	Arg	Gly	Glu	Glu	Arg	Asp	Leu		
	115					120					125						
gac	cac	gag	atg	ctc	gcc	ctc	tcc	ctg	cgc	ctc	ctc	ggg	cgg	gcc	ctc	432	
Asp	His	Glu	Met	Leu	Ala	Leu	Ser	Leu	Arg	Leu	Leu	Gly	Arg	Ala	Leu		
	130					135					140						
ttc	ggg	aag	ccc	ctc	tcc	cca	agc	ctc	gcg	gag	cac	gcc	ctt	aag	gcc	480	
Phe	Gly	Lys	Pro	Leu	Ser	Pro	Ser	Leu	Ala	Glu	His	Ala	Leu	Lys	Ala		
	145				150				155					160			
ctg	gac	cgg	atc	atg	gcc	cag	acc	agg	agc	ccc	ctg	gcc	ctc	ctg	gac	528	
Leu	Asp	Arg	Ile	Met	Ala	Gln	Thr	Arg	Ser	Pro	Leu	Ala	Leu	Leu	Asp		
				165				170						175			
ctg	gcc	gcc	gaa	gcc	cgc	ttc	cgg	aag	gac	cgg	ggg	gcc	ctc	tac	cgc	576	
Leu	Ala	Ala	Glu	Ala	Arg	Phe	Arg	Lys	Asp	Arg	Gly	Ala	Leu	Tyr	Arg		
			180					185				190					
gag	gcg	gaa	gcc	ctc	atc	gtc	cac	ccg	ccc	ctc	tcc	cac	ctt	ccc	cga	624	
Glu	Ala	Glu	Ala	Leu	Ile	Val	His	Pro	Pro	Leu	Ser	His	Leu	Pro	Arg		
		195					200					205					
gag	cgc	gcc	ctg	agc	gag	gcc	gtg	acc	ctc	ctg	gtg	gcg	ggc	cac	gag	672	
Glu	Arg	Ala	Leu	Ser	Glu	Ala	Val	Thr	Leu	Leu	Val	Ala	Gly	His	Glu		
	210					215					220						
acg	gtg	gcg	agc	gcc	ctc	acc	tgg	tcc	ttt	ctc	ctc	ctc	tcc	cac	cgc	720	
Thr	Val	Ala	Ser	Ala	Leu	Thr	Trp	Ser	Phe	Leu	Leu	Leu	Ser	His	Arg		
	225				230					235					240		
ccg	gac	tgg	cag	aag	cgg	gtg	gcc	gag	agc	gag	gag	gcg	gcc	ctc	gcc	768	
Pro	Asp	Trp	Gln	Lys	Arg	Val	Ala	Glu	Ser	Glu	Glu	Ala	Ala	Leu	Ala		
				245				250						255			
gcc	ttc	cag	gag	gcc	ctg	agg	ctc	tac	ccc	ccc	gcc	tgg	atc	ctc	acc	816	
Ala	Phe	Gln	Glu	Ala	Leu	Arg	Leu	Tyr	Pro	Pro	Ala	Trp	Ile	Leu	Thr		
			260				265						270				
cgg	agg	ctg	gaa	agg	ccc	ctc	ctc	ctg	gga	gag	gac	cgg	ctc	ccc	ccg	864	
Arg	Arg	Leu	Glu	Arg	Pro	Leu	Leu	Leu	Gly	Glu	Asp	Arg	Leu	Pro	Pro		
		275					280					285					



ggc acc acc ctg gtc ctc tcc ccc tac gtg acc cag agg ctc cac ttc 912  
 Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe  
 290 295 300  
  
 ccc gat ggg gag gcc ttc cgg ccc gag cgc ttc ctg gag gaa agg ggg 960  
 Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly  
 305 310 315 320  
  
 acc cct tcg ggg cgc tac ttc ccc ttt ggc ctg ggg cag agg ctc tgc 1008  
 Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys  
 325 330 335  
  
 ctg ggg cgg gac ttc gcc ctc ctc gag ggc ccc atc gtc ctc agg gcc 1056  
 Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala  
 340 345 350  
  
 ttc ttc cgc cgc ttc cgc cta gac ccc ctc ccc ttc ccc cgg gtc ctc 1104  
 Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu  
 355 360 365  
  
 gcc cag gtc acc ctg agg ccc gaa ggc ggg ctt ccc gcg cgg cct agg 1152  
 Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg  
 370 375 380  
  
 gag gag gtg cgg gcg cat cac cat cat cat cac tga 1188  
 Glu Glu Val Arg Ala His His His His His His  
 385 390 395

<210> 6

<211> 395

<212> PRT

<213> Artificial sequence

<223> Description of the artificial sequence: C-terminal  
His-tagged

<400> 6

Met Lys Arg Leu Ser Leu Arg Glu Ala Trp Pro Tyr Leu Lys Asp Leu  
1 5 10 15

Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro  
20 25 30

Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp  
35 40 45

Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala  
50 55 60

Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu  
65 70 75 80

Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp  
85 90 95

Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu  
100 105 110

Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu  
115 120 125

Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu

130	135	140
Phe Gly Lys Pro Leu Ser	Pro Ser Leu Ala Glu His Ala Leu Lys Ala	
145	150	155 160
Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp		
	165	170 175
Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg		
	180	185 190
Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg		
	195	200 205
Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu		
	210	215 220
Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg		
	225	230 235 240
Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala		
	245	250 255
Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr		
	260	265 270
Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro		
	275	280 285
Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe		
	290	295 300
Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly		
	305	310 315 320
Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys		
	325	330 335
Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala		
	340	345 350
Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu		
	355	360 365
Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg		
	370	375 380
Glu Glu Val Arg Ala His His His His His His		
	385	390 395

&lt;210&gt; 7

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence: PCR primer

&lt;400&gt; 7

cgaagctcat atgaagcgcc tttccctgag

<210> 8  
 <211> 30  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence: PCR primer

<400> 8  
 gcgaattcac gcccgcacct cctccctagg 30

<210> 9  
 <211> 42  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence: PCR primer

<400> 9  
 cgaagctcat atgcatcacc atcatcatca caagcgcctt tc 42

<210> 10  
 <211> 42  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence: PCR primer

<400> 10  
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<210> 11  
 <211> 30  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence: PCR primer

<400> 11  
 ccggaattca tgaagcgcct ttccctgagg 30

<210> 12  
 <211> 44  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence: PCR primer

<400> 12  
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